

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 12:21:43 ; Search time 90 Seconds

(without alignments)
8430.418 Million cell updates/sec

Title: US-10-082-894-1

Perfect score: 1719

Sequence: 1 gtttaattaccgaatttga.....aaatctcgttataaaaatt 1719

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCrUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295.8	17.2	1566	4. US-09-328-352-1297	Sequence 1297, Ap
2	284.8	16.6	580073	4. US-08-545-528D-1	Sequence 1, Appli
3	271.2	15.8	1554	4. US-09-134-001C-2607	Sequence 2607, Ap
4	153.2	8.9	1557	4. US-09-252-991A-6920	Sequence 6920, Ap
5	153.2	8.9	1590	4. US-09-252-991A-6824	Sequence 6824, Ap
6	105.4	6.1	741	4. US-09-252-991A-6774	Sequence 6774, Ap
7	95.2	5.5	2094	3. US-08-714-918-87	Sequence 87, Appl
8	95.2	5.5	2094	3. US-09-265-315-87	Sequence 87, Appl
9	95.2	5.5	2094	3. US-09-265-315-87	Sequence 87, Appl
10	95.2	5.5	2094	3. US-09-266-417-87	Sequence 87, Appl
11	81.4	4.7	484	3. US-08-975-762-34	Sequence 34, Appl
12	81.4	4.7	484	3. US-08-821-324-34	Sequence 34, Appl
13	81.4	4.7	484	3. US-09-295-028-34	Sequence 34, Appl
14	81.4	4.7	484	3. US-09-106-582-34	Sequence 34, Appl
15	39.8	2.3	2861	4. US-09-398-395A-55	Sequence 55, Appl
16	39.8	2.3	2861	4. US-09-887-586A-55	Sequence 55, Appl
17	39.8	2.3	2861	4. US-09-895-752-55	Sequence 55, Appl
18	39.8	2.3	2861	4. US-09-903-012B-55	Sequence 55, Appl
19	37.8	2.2	521	4. US-09-669-751-138	Sequence 138, App
20	37.8	2.2	864	4. US-09-601-198-85	Sequence 85, Appl
21	37.4	2.2	1329	4. US-09-134-001C-196	Sequence 196, App
22	36.6	2.1	3095	6. 5231168-1	Patent No. 5231168
23	36.4	2.1	1557	4. US-09-134-001C-1614	Sequence 1614, Ap
24	36.2	2.1	319608	4. US-09-679-409-1	Sequence 1, Appli
25	36.2	2.1	1664976	4. US-08-916-421B-1	Sequence 1, Appli
26	36.2	2.1	1664976	4. US-08-916-421B-1	Sequence 1, Appli
27	36	2.1	729	3. US-08-998-416-1031	Sequence 1031, Ap

28	35.8	2.1	319608	4. US-09-539-333D-1	Sequence 1, Appli
29	35.6	2.1	2088	4. US-09-328-352-624	Sequence 624, App
30	35.4	2.1	648	4. US-09-328-352-2915	Sequence 2915, Ap
31	35.4	2.1	6027	2. US-08-968-542C-1	Sequence 1, Appli
32	35.4	2.1	6216	3. US-09-213-053-1	Sequence 1, Appli
33	35.2	2.0	2355	4. US-08-913-159-12	Sequence 12, Appli
34	35.2	2.0	29793	4. US-09-302-812-38	Sequence 38, Appli
35	35.2	2.0	29793	4. US-09-511-477-38	Sequence 38, Appli
36	35.2	2.0	29793	4. US-09-511-507-38	Sequence 38, Appli
37	34.8	2.0	1200	4. US-09-328-352-3506	Sequence 3506, Ap
38	34.8	2.0	1311	3. US-08-584-760A-66	Sequence 66, Appli
39	34.6	2.0	12286	4. US-09-322-478-17	Sequence 17, Appli
40	34.6	2.0	12571	4. US-09-322-478-20	Sequence 20, Appli
41	34.4	2.0	366	4. US-09-134-001C-2003	Sequence 2003, Ap
42	34.4	2.0	1380	4. US-09-134-001C-2019	Sequence 2019, Ap
43	34.4	2.0	4383	6. 5175095-4	Patent No. 5175095
44	34.4	2.0	580073	4. US-08-545-528D-1	Sequence 1, Appli
45	34.2	2.0	1446	4. US-09-601-198-140	Sequence 140, App

ALIGNMENTS

RESULT 1

US-09-328-352-1297

; Sequence 1297, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328.352

; CURRENT FILING DATE: 1998-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 1297

; LENGTH: 1566

; TYPE: DNA

; ORGANISM: Acinetobacter baumannii

US-09-328-352-1297

Query Match 17.2%; Score 295.8; DB 4; Length 1566;
Best Local Similarity 55.4%; Pred. No. 8.3e-72;
Matches 702; Conservative 0; Mismatches 547; Indels 18; Gaps 6;

Qy	178	GGTCTTCATGTTGATGCCAGAGGCTTAATGGAAATCTGAAGTTGGACATTTGAAT	237
Db	178	GGTGAAGATGTTGGTTTACCTGATGGACAAATGGTAACCTCGGAAGTTGGTCACATGAAC	237
Qy	238	ATAGGAGCTGGAAGAGTTATTTATCAAGATATTCTGGAATTAATTTGGCTGTTCACAGA	297
Db	238	CTTGCGCTGGCCGAGTGTATACCAAGACTTCACACGTATTACTAAGATATTTCGTACT	297
Qy	298	AACGAGTTTGTACAAATCTCAGATTGTCATCAGCTAGCTGAGCGTGCAGAAAGGGGAGT	357
Db	298	GGTCTTTTGTAGCAGCAAGATATTGTTGATGCCGTAGAAAAAGCAAGACGACGGGT	357
Qy	358	GGTCGATGCTATTTAGGACTGGTTAGCCACTGGTGCTCCACTCTCATATTGATCAT	417
Db	358	GGTCGATGCTATTTAGGACTGGTTAGCCACTGGTGCTCCACTCTCATATTGATCAT	417
Qy	418	CTTTTTCGGTGTGATGCTGCTATTTAAACAATTAACAAGTGCCAAAGGTTTTCATTCAC	477
Db	418	ATTCTGGC---GATGTGTGACTTTCCTTAAACCGCGTGCAGAAAGTTTACTTACATGCA	474
Qy	478	TTTGCTGATGCTGAGATACCTTCGCCAACAAAGTGAGCTGGTTATCTCTGAAACACTTCT	537
Db	475	TTCTTGTATGCTGCTGACACTCCCTCCACGTAGTGTCTCAACCTTCATTTAGAAAAATAGAC	534
Qy	538	CAATTATTGCT---TCGAAAAAGTACGGAGAAATGGCTACTATTACTGGACGTTATTAT	594
Db	535	GCATTATTCGCTAAATATCCGAACAGGCGGTATTGCAACCATGATTTGGTGGCTATTTT	594

595	Qy	GCAATGGATAGGACAAAAGATGGGACCGTATTAAAGATGGCTTATGAGCAATTTGTGGA	654
595	Db	GCAATGGATCGTGATAACCGTTGGGATCGTTGAGCAGCGTTTACCCTTTATTAAACGGAA	654
655	Qy	GGTATTTGGACAAAAGCCACCGTTGATAAGAGCTGTCGATGCTTGTAGAGAGCCATATGCT	714
655	Db	GG---TGAAGCTGTCGTACTGCAATATACTCGGGTTGAAGGCTTAGAGCTTGCGATATGCT	711
715	Qy	CAATCTGAGACTGACGAATTTCTGAAACCAATTTGTTTTTGGACAGCATGGCGAGTAAAA	774
712	Db	GCAAAATGAAAATCATGAGTTTGTAAAAGCAACTCGTATTGGTCGAGATCGCTAAAGTTCAA	771
775	Qy	GATGACGATACTCTTATTTCTTCAATATATCGTGCTGATCGGTATGCGTCAAAATTTGTGAA	834
772	Db	GATGGCGATAGTGTGTATATATGAAATTTTCGCTGACGCTGCCGCTGAAATATACGCGT	831
835	Qy	TGTTTTGGGCTCTCAACGTTATAAAGATCTTAATAGTTTCGGTTCCCTCACCCCTAAAAATATT	894
832	Db	CGCTTTGTGAAAAGAGTTTCGCGAGGTTTGGACGCTAAAGTTGTACA--GAACCTTTCT	888
895	Qy	CAGATTAGTGGGATGACCAATACAAATAAGAGTTTCCATTTCCATCGTTATTTCCACCT	954
889	Db	AAATTTGTCTATGTTGACGGCTTATCAGGCAAGTATTGATCGCACCTGTGGCATATATGCCT	948
955	Qy	GTGACTCATACTAATGTCTGTGATGCGTTCTTCAAGGAGCTTACTCAATTTTCAC	1014
949	Db	GAAGAGTTAAAGAACTCGCTGTGTGTAATATTATATCTTTTAGTTAAACGCAACTACGT	1008
1015	Qy	TGTGCGAAACTGAGAAGTATCCTCATGTTACCTTCTTTAATGGTGGTCGAGAAGTT	1074
1009	Db	ATTGCTGAAACTGAGAAATATGCCATGTGACTTTCTTTAGTGGTCGTGAAGAC	1068
1075	Qy	CAATTTCCAAGATGAAGCGGTTGATGGTTCCCTGACCAAAAGAAAGTTGCTACATATGAT	1134
1069	Db	GAATATCCAGGTGAAAAGCGTATTTTAATTCATCACCAA---ACGTTGCGACATATGAC	1125
1135	Qy	TTAAAAACCAGAAATGAATGCTGTGGAGTTGCCGAAAAAATGGTCGAGCAAAATAGTCA	1194
1126	Db	TTAAAGCCTGAAATGAGTGCTTATGAAGTAACGTGATGAGCTAGTCAAGCAATTAAGTCG	1185
1195	Qy	GGCAGGATCCCTTTGGTTATGTGCAATTTTGGCCCTCTGACATGGTTGGACATATCGTT	1254
1186	Db	GGTGATACGACTTACTTGTGTGAATCTATGCCAATGGTGATATGGTCGTGCATACAGGC	1245
1255	Qy	AAATTTGAACCTGCCCTCAAAGCATCTCAAGCTACTGACGAGGCAATTGGAAAGATATTT	1314
1246	Db	GTATTTGATGCTGCAGTTTAAAGCCGTTGAAGCAAGTTGATACATGTTTAGTCGTGTATAC	1305
1315	Qy	GAGCATGCCAACTTATTAATTACGTTCTTATGGTTACTTTCOGATCATGGAATCTGTGAG	1374
1306	Db	GAACTGTAAATGCGAAAAAAGGCCATATGCTTATTACGGCTGACCAACGGTAATGTGAA	1365
1375	Qy	AAGATCATGCTCCCA---TGGTAGTGAACATCTGCATACCTGCAATTTGGTCCCA	1431
1366	Db	CAAAATGCAAGATTATGAAAGTTGGTCAGGTTTCATACTCAGCATACAAACAGAGCTTGGCT	1425
1432	Qy	TTTACTT	1438
1426	Db	TTTATTT	1432

RESULT 2

US-08-545-528D-1/c
: Sequence 1, Application US/08545528D

; Patent No. 6537773
; GENERAL INFORMATION:

APPLICANT: Fraser
TITLE OF INVENTION:

Patent No. 6537773

```

; PRIOR APPLICATION NUMBER: US 08/488,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

```

; AFFRICANI, ROSELI ET AL.;
 ; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
 ; Patent No. 6537773
 ; TITLE OF INVENTION: Thereof, and Uses Thereof
 ; FILE REFERENCE: PB193P1
 ; CURRENT APPLICATION NUMBER: US/08/545,528D
 ; CURRENT FILING DATE: 1995-10-19

Db 536731 CTGAATGAAAGAAAGAAATTTATTTTGTAGCAATGATGATATGAGGGAATTG 536672
Qy 929 TTCCATTTCCATCGTTATCCACCTGTGACTCATACTAATAGTGTGCTGGAATGGCTTG 988
Db 536671 TACCTAGCAATTTGCTTTTCCACCTCAAAACCAATTAATAATAGTCTTGGTGAAGTAATG 536612
Qy 989 CTTCTCAGGAGTTTACTCAATTTCCACGTGCGGAACTGAGAGTATCCTTCATCTTACCT 1048
Db 536611 CTAATAATAATTTGAACCAATTTGAGGATTCGAGAACTGAAGATGCTTCACGTTACTT 536552
Qy 1049 TCTTCTTAATGPGGTGCGAGAGTTTCAATTTCCAAAGATGAAGAGCGTTGTATGTTCCGT 1108
Db 536551 TCTTTTGTGTTGTTGTTTGAAGTTAATCTCAGCAATGAACAAAGACATTAATCTCTT 536492
Qy 1109 CACCAAAAGAGTTGCTACATATGATTTAAACCCAGAAATGAATGCTGCTGGAGTTGCCG 1168
Db 536491 CTTTAA---AAGTTGTACATATGATTTAGCTCCCGAAATGTCAATGAAGCTATTACTG 536435
Qy 1169 AAAAATGGTCGAGCAAAATGAGTCAGGAGGCATCCTTTGGTTATGTGCAATTTTGGC 1228
Db 536434 ATGCACACTAGAAAAGCTTAA-----TAACTTTGATTTTACTGTTTAAATTTGCTA 536381
Qy 1229 CTCTGACATGGTTGGACATCTACTGGTAAATTTGAACCTGCCGTCAAGACATGTCAAGCTA 1288
Db 536380 ATCTGTATATGTTAGGTCACTACTGGTAACTATCAAGCTTGCATTAAGCTTCTTGAAGCAC 536321
Qy 1289 CTGACGAGCAATTTGGAAGATATTTGAAGCATGCCAACTTATAATACGTTCTTTATGG 1348
Db 536320 TCGATGTTCAAAATTAACGAATATGTTGATTTTGAAGCTAACTCAATCAATCAATGTTT 536261
Qy 1349 TTACTTCGATCATGGAATGCTGAGAGATGATTTGCTCCGATGGTAGTGAACATACTG 1408
Db 536260 TAATCGACATCATGGAATGAGAGTGAAGTGAATGATATAATAACAACTTACTA 536201
Qy 1409 CACATACCTGCAATTTGGTCCCAATTTACTTCTCTTCCAAACAACTTTGTTTTTAAATCGA 1468
Db 536200 AACACATTAATAATCCCTGTACCAATTTGTATGTACTGACAAAAATGTTAACTTTAATCAAA 536141
Qy 1469 CT 1470
Db 536140 CT 536139

RESULT 3

US-09-134-001C-2607
; Sequence 2607, Application us/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134.001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 2607

; LENGTH: 1554

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2607

Query Match 15.8%; Score 271.2; DB 4; Length 1554;

Best Local Similarity 51.4%; Pred. No. 5e-65;

Matches 759; Conservative 0; Mismatches 703; Indels 16; Gaps 5;

Qy 12 CAAGTTTGAGATGACCAATATCAAAATGTTCAACAAAGATCTGTCTTT-CTAGTTATG 70

Db 11 CAATTTGTAAGGTGCAAAATATATGCAAAACCAACTGCCTTAATCATCTATG 70

Qy 71 ATGATGGGCGCTTTCGATGAACAACACGGAATGCAATTTGCTTAAAGCTTAAACGCCTA 130
Db 71 ATGTTTCGCAATTCGTAAGATGACATGCGCAATGCGTTAAGCAAGACACATAACCTA 130
Qy 131 TTATGGACAAACTTTGTTCTGGAAATTTGGCAAAA---AATTGGAGACACACGGTCTTCATG 187
Db 131 ATTTGTATCATATATGAAAAATATCTCAACACAAATAGAACTAGTGGCTTAGATG 190
Qy 188 TTGGATTGCCAGAGGCTTAATGGGAAATTTCTGAGTTGGACATTTGCAATATAGGAGCTG 247
Db 191 TAGGTTCTCTGAGAGTCAAAATGGGTAACTCTGAAGTAGGACATATGAAATATTGGTGCAG 250
Qy 248 GAAGAGTTATTTATCAAGATATTTCTGAAATTAATTTGGCTGTCAACAGAAACGAGTTTG 307
Db 251 GACGCATCGTATATCAAGTTTAACTCGTATTAATAATCGATTGAAGACGGAATTTCT 310
Qy 308 TTACAAATCTCAGATTTGTCATGAGCTGAGCGTGCAAGAGAGGGAGTGGTGCATGTC 367
Db 311 TTGATAACACTGTATTAATAAACACTGTAAACATGTTAAAGACAATGGCTCTCGCTTC 370
Qy 368 ATTTATTAGACTGGTTAGCGATGGTGTCCACTCTCATATTGATCATCTTTTTCGGT 427
Db 371 ATGATTTTCGATTTCTGATGGTGTGTACACAGCTCATTTAAGCATCTTATTTGCTA 430
Qy 428 TGATACGTGCTATTTAAACAATTTACAAGTGCACAAAGTTTTCATTCACCTTTTTCGTGATG 487
Db 431 TTTTGAATTTAGCTTAAAGCAAGGAATAGATAAGTATATGTCACGCACTTTTATGATG 490
Qy 488 GTCGAGATCTTCCCAACAGTGGAGCTGGTATCTTTGAACAACACTTCTTCAATTTATG 547
Db 491 GTCGTGATGTTGATCAAAAATCTGTTTGAATAATATAGAGAACTGAAGATAAATTTA 550
Qy 548 CTTCCGAAAGTAGTCGGAGAATTTGCTACTATTACTGACGCTTATATGCAATGATAGG 607
Db 551 AAGAAATTTAGGTAGGCAATTTGCTTCTGTTTCAGGACGTTATATGCTATGACCGGTG 610
Qy 608 ACAAAAGATGGAGCGCTATTAAAGATGGCTTATAGGCAATTTGTTGGAGTATTGGACAAA 667
Db 611 ACAAGCTTGGGATCGTGAGGAACGTCCTATATANTGCTATTTTCGTAACCTTTTGAAGTCTCCTA 670
Qy 668 AAGCCACGTTGATAAGGCTGTCGATGTTGTTAGAGAGCGATATGCTCAATCTGAGACTG 727
Db 671 CATTTACTTCAGCTTAAAGCAGCGCTTGAAGCTAATTTAATAAATGATGTGACTGATGAAT 730
Qy 728 ACGAATTTCTGAACCAATTTGTTTTCGGACGATGGCGAGTAAAGATGACCATCTC 787
Db 731 TCGTCGAACCGTTTATAGTTGAAGCCCAAAACGATGGT---GTGAACGATGGAGCGGAG 787
Qy 788 TTATTTCTTCAATATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 847
Db 788 TAATCTTTTATATTTCCGTCACAGATAGAGCAGCTCAACTTTTCAGAAATCTTTACTAATA 847
Qy 848 AACGTTATAAGATCTTAATAGTTTCGCTTCCCTCACCTTAAATAATTCAGATTTAGTGGGA 907
Db 848 AAGCGTTTGTATGATTTAA-----AGTTGAACAAGTGGACAACCTTATTTCTACGCTACAT 901
Qy 908 TGACCCCAATCAATTAAGAGTTTCCATTTTCATGCTTATTTCCCTGCTGCTGCTGCTGCTGCT 967
Db 902 TCAGGAAATATAATGACAATGTAGATGCTGAAATTTGTAATAAGAGTTGACTTTAAATA 961
Qy 968 ATGTGCTTGTGTAATGGCTTCTTCTCAAGGAGTTTACTCAATTTTCACTGTGCGGAAACTG 1027
Db 962 ATACAATCGGTGAAGTTGCTCAAGATATGCTTGAACAAATACGTTATCGTGAACACTG 1021
Qy 1028 AGAAGTATCCCATGTTTACCTTCTTCTTAAATGTTGGTGGAGAGTTCATTTCCAAAGATG 1087
Db 1022 AAAAGTATCCCATGTTTAACTACTTTATGAGTGGTGGAGCAAAATGAAGAGTTTGAAGGAG 1081
Qy 1088 AAGAGCGTTGTATGTTTCCCGTCCACCAAGAAAGTGTGCTACATATGATTTAAACCCAGAAA 1147
Db 1082 AACGTCGTAGACTCATCGATTTCTCAA---AAGTAGCGACTTATGATTTAAACCTGAGA 1138

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6824
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6824

Query Match 8.9%; Score 153.2; DB 4; Length 1590;
Best Local Similarity 47.9%; Pred. No. 1.6e-32;
Matches 582; Conservative 0; Mismatches 613; Indels 21; Gaps 4;

QY 177 CGGTCTTCATGTTGGATTGCCAGAGGCTTAATGGGAAATTCGAAGTTGGAGATTGAA 236
DB 192 CGCATGGAGTCGGCTGCCACGCCAGATGGCAATTCGGAGTCCGCCACATGAA 251
QY 237 TATAGGAGCTGGAAGAGTTATTATCAAGATATTGTTGGAATTAATTTGGCTGTCAACG 296
DB 252 CCTCGCGCAGCGCGGTGTGTACAGGACTTCCCGCGGTACCAAGGCCATTCGCCGA 311
QY 297 AAACAGATTGTTTACAAATCCTCAGATTTGTGCATCAGCTGAGCGTGCAGAAAGGGGAG 356
DB 312 CGCGGAATTTTCGAAACCCGGTGTATCGCGCGGGGTGCGACAAAGCCGTCGCCGCCGA 371
QY 357 TGGTCGATTCATATTAGGACTGGTTACGATGGTGGTGTCCACTCTCATATTGATCA 416
DB 372 CAAGCGGTGCACATCTCGCTGCTCTCCCGCGCGGTGTACACAGCCATGAAGACCA 431
QY 417 TCTTTTTCGCTGTATAGCTGCAATTTAAACAATTAAGTCCCAAGGTTTTCATTCACCT 476
DB 432 CTGTGTCGAATGCGCGAGATGCGCCCAAGCGCGCGCGGCAAGATCTACTGTGATGC 491
QY 477 TTTGCTGATGGTCGAGATACTTCGCCAACAAGTGGAGCTGGTATCTTGAACAACATCT 536
DB 492 CTCTCTGATGGCGCGATACCCCGCGGAAAGCGCGCGTGTGCGTGGAGCGTCTCGA 551
QY 537 TCAATTTATTTGCTTCGGAAGTACGGAGAAATTTGGTACTATTACTGGAGCTTATATGC 596
DB 552 CGCCACCTTCGCGCGGCTCGGCAAGGCGCGCATCGCTCGATCATCGGCGCTATTTCGC 611
QY 597 AATGATAGGACAAAGATGGAGCGTATTAAAGTGTATGAGGCAATTTGTTGGAG 656
DB 612 GATGGACCGGACACCGCTGGACCGCTCGAGCGCGCTCGAGCGCGCTACGCCCG 728
QY 657 TATTGGACAAAGACCCCGCTTGATAGGCTGTCGATGTTGTTAGAGAGCGATATGCTCA 716
DB 672 CAAGCGCGAGTT---CACC CGCGACTCTCGGTGGCAGCCCTCGAGCGCGCTACGCCCG 728
QY 717 ATCTGAGACTGACGAATTTCTGAACCAATTTGTTTTT-----CGAGCATGG 764
DB 729 CGCGGAGAGCGCAATTCGTAAGGCGCACCGCGGTGTCCCGCGCGCGCGCAAGCGGT 788
QY 765 GCGAGTAAAGATGACCATCTCTATTTCCTCAATTAATCGTGTCTGATGCTATGCTCA 824
DB 789 GCGGTGCGAGATGGCGACCGGTGATCTTCATGAACTTCGCGCGCGCGCGCGCGCG 848
QY 825 AATTTGTAATGTTGGGTCTCGAACCGCTTAAAGATCTTTAATAGTTTCGTTCCCTACCC 884
DB 849 GCTGAGCGCGCTTCG---TCGAGCGCGCATCAATGAGTTCCCGCGCGAAGCGCGCC 905
QY 885 TAAATAATTCAGATTTAGTGGATGACCAATCAATAAGAGTTTCCATTTCCATCGTT 944
DB 906 GCAGCTGGCAGGTTTCTGATGCTGACCCAGTAGCGCGCGAGCATCCCGCGCGCTCGC 965
QY 945 ATTCCCACTGTGACTCATACTAATGCTGTGTAATGCTGTGCTTCTCAAGGATTC 1004
DB 966 CTTCGCCCGGAGCGGTGACCAACGTCCTCGCGGAGTACTTGGCCCAAGCATGGCAAGC 1025
QY 1005 TCAATTTCACTGTGCGGAACTGAGAAATGATCTCTCATGTTTACCTTCTTTAATGTTG 1064

DB 1026 CCAGCTGCGCATCGCGGAGACCGAGAGTACGCCCATGTGACCTTCTCTTCTCCGCGG 1085
QY 1065 TCGAGAAGTTCAATTCAGATGAAGAGCGTTGTATGTTCCGTCCACCAAGAAAGTTGC 1124
DB 1086 CCGCAGGAAACCCCTACGAGGCGGAGGAGCATCTCTGATCCCTCGCGCA---AGGTCCG 1142
QY 1125 TACATATGATTTAAACACAGAAATGAATGCTGCTGGAGTTGCCGAAAAAATGTCGAGCA 1184
DB 1143 CACCTAGACCTGCACCCGAGATGAGCGCGCGGAAGTACCAGACCGTATGTCGAGGC 1202
QY 1185 AATTGAGTCAGGAGGCATCTTTTGGTTATGTCAATTTTTCGCTCTCTGACATGTTGG 1244
DB 1203 CATCGAGCAACAGCGCTACGACGTGATCGTGTGCACTACGCCCAACGCGACATGGTCGG 1262
QY 1245 ACATAGTGGTAAATTTGAACCTGCCGTCAAGCATGTCAAGCTACTACGAGGCAATGG 1304
DB 1263 CCACCGGGGTGTTGAGGCGCGGTCTAGGCGGTGAGTGGCTGGACACCTGTCATGGG 1322
QY 1305 AAAGATATTTGAAGCATGCCAAACTTAATTAATTAAGTTTCTTTATGGTTACTTCCGATCATGG 1364
DB 1323 CGGTATGTCGAGCGCTGCACAGGTGCGGCGGAAGCCCTGATCACC CGCGACCGG 1382
QY 1365 AATGCTGAGAAGATG 1380
DB 1383 CAATGTCGAGCAGATG 1398

RESULT 6

US-09-252-991A-6774
; Sequence 6774, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 6774
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6774

Query Match 6.1%; Score 105.4; DB 4; Length 741;
Best Local Similarity 52.5%; Pred. No. 1.7e-19;
Matches 279; Conservative 0; Mismatches 246; Indels 6; Gaps 2;

QY 906 GATGACCAATAACAATAAGAGTTTCCATTTCCATCTGTTATCCACCTGTGACTCATAC 965
DB 43 GCTGACCCAGTACGCGCGAGCATCCGCGCGCTCGCGCTTCCCGCGGAGCGCGTGAC 102
QY 966 TATGCTGCTGTAATGGCTTGTCTCTCAAGAGTTACTCAATTTCACTGTGCGGAAAC 1025
DB 103 CAACGTCTCGGGAGTACCTGGCCAAAGCATGGCAAGACCGACGTGCGCATCGCGGAGC 162
QY 1026 TGAGAAGTATCCCTCATCTTACCTTCTTTTAAATGTTGGTGGAGAGTTCAATTTCCAGA 1085
DB 163 CGAGAAGTACGCCCATGTGACCTTCTTCTTCTCGCGCGCGCGGAGAACCTTACGAGG 222
QY 1086 TGAAGACGTTGTATGTTTCCGTCCCAACAAAGAGTTGCTACATATGATTTAAACACGA 1145
DB 223 CGAGGACCGCATCTCTGATCCCTCGCGCA---AGGTGCGCCACTTACCACTGCAACCGA 279
QY 1146 AATGAATGCTGCTGAGTGTCCGAAAAAATTTGGTGCAGCAAAATTTGAGTCAGGACGATCC 1205
DB 280 GATGAGCGCGCGGAAGTACCCGACCGCTATCTGTCGAGGCCATCGAGCAACAGCGCTACGA 339

Matches	211; Conservative	0; Mismatches	194; Indels	0; Gaps	0;
Qy	196	CCAGAAAGCGTTAATGGGAAATCTCGAAGTTGGACATTTGAATATAGAGCTGGGAAGATT	255		
Db	1690	CTTGAAGGACAAATGGTAACTCAGAAGTTGGTCATATGAATTCGGTCAGGACGATATC	1749		
Qy	256	ATTATATCAAGATATTGTTCCGAATTAATTTGGCTGTTTCAACGAAACAGATTGTTTCAAAAT	315		
Db	1750	GTTTATCAAAAGTTTAACTCGAATCAATAATCAATTTGAAGACGGTGATTCTTTTGAATAAT	1809		
Qy	316	CCTCAGATTTGTCATCAGCTGAGCGTGCGAAAGGGGAGTGCTGATTCATTTTATTATTA	375		
Db	1810	GATGTTTTAAATTAATGCAATTGCACAGTGAATTCACATGATTCACGGTTACACATCTTT	1869		
Qy	376	GGACTGGTTAGCGATGGTGTCCTACTCTCAATATTGATCATCTTTTTGGTTGTACAGT	435		
Db	1870	GGTTTATTGTCTCAGCGTGGTGTCACAGTCATACAAACATTTATTTGCTTTGTTAGAA	1929		
Qy	436	GCATTTTAAACAATTACAAGTGCCAAAGGTTTTTCATTTTCACTTTTTTCTGATGTCGAT	495		
Db	1930	CTTGTCTAAAAAACAGAGTGTTGAAAAGTTTACGTACACGCAATTTTATGATGCCGTGAC	1989		
Qy	496	ACTTCGCCAACAAAGTCGAGCTGGTTATCTTTGAACAACATCTCTTCAATTTATTTGCTTCGGAA	555		
Db	1990	GTAGATCAAAAATCCCGCTTTGAATATACATCGAAGACATGAAGCTAAATCAATGAATTA	2049		
Qy	556	AAGTACGGAGAATTGGCTACTATTACTGGACGTTATTATGCAATG	600		
Db	2050	GGCATTTGGTCAATTTGCATCTGTGCTGGTCGTTATTATGCAATG	2094		

RESULT 8
US-09-265-315-87

US-05-203-313-87
: Sequence 87, Application US/09465315
: Patent No. 6187541
: GENERAL INFORMATION:
: APPLICANT: Benton, Bret
: APPLICANT: Lee, Ying J.
: APPLICANT: Malouin, Francois
: APPLICANT: Martin, Patrick K.
: APPLICANT: Schmid, Molly B.
: APPLICANT: Sun, Dongxu
: TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
: TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
: TITLE OF INVENTION: TARGET GENES
: NUMBER OF SEQUENCES: 111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/265,315
: FILING DATE: March 9, 1999
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/714,918
: FILING DATE: September 13, 1996
: APPLICATION NUMBER: 60/009,102
: FILING DATE: December 22, 1995
: APPLICATION NUMBER: 60/003,798
: FILING DATE: September 15, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.

Query Match	5.5%;	Score 95.2;	DB 3;	Length 2094;
Best Local Similarity	52.1%;	Pred. No. 1.8e-16;		

APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 2094 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-87

Query Match 5.5%; Score 95.2; DB 3; Length 2094;
Best Local Similarity 52.1%; Pred. No. 1.8e-16;
Matches 211; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 196 CCAGAGGCTTAATGGGAATTCGAAAGTTGGACATTTGAATATAGGAGCTGGAAGAGTT 255
Db 1690 CCTGAAGGACAAATGGGTAACTCAGAAAGTTGGTCATATGAATATCGTGCAGGACGTATC 1749
QY 256 ATTATACAGATATTTCTCGAATTAATTTGGCTGTTCAACGAACAGAGTTGTTACAAAT 315
Db 1750 GTTATCAAGTTTAACTCGAATCAATAAATCAATTAAGAGCGGTGATTTCTTTGAAAAT 1809
QY 316 CCTCAGATTTGTCATCAGCTGAGCTGCAAGAGAGGGAGTGGTCGATTTATTA 375
Db 1810 GAATGTTTAAATGAATTCGACAGTGAATTCATGATGATTCAGCGGTACACATCTTT 1869
QY 376 GGACTGGTTAGGATGGTGGTGTCCACTCTCATATTTGATCATCTTTTTCGTTGATACGT 435
Db 1870 GGTATTTGCTGACGGTGGTGTACACAGTCATTAACAATTTATTTCTTTGTTAGAA 1929
QY 436 GCATTTAAACATTAACAAGTGCAGAGTTTTCATTCATCTTTTTCGTCGATGGTGCAGAT 495
Db 1930 CTTGCTAAAAACAAGGTGTTGAAAAAGTTTACGTACAGCATTTTATAGTGGCGGTGAC 1989
QY 496 ACTTCCCAACAAGTGGAGCTGGTTATCTTGAACAACCTCTTCAATTTTATGCTTCGGAA 555
Db 1990 GTAGATCAAAATCCGCTTTGAAATACATCGAAGAGACTGAAGCTAAATTCATTAATTA 2049

QY 556 AAGTACGGAGAAATGGCTACTATTAATGACGTTATATGCAATG 600
Db 2050 GGCAATGGTCAATTTGCACTGTCTGCTGCTGCTATATGCAATG 2094

RESULT 11

US-08-975-762-34/c
Sequence 34, Application US/08975762
Patent No. 6207169
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,762
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-08-975-762-34

Query Match 4.7%; Score 81.4; DB 3; Length 484;
Best Local Similarity 53.4%; Pred. No. 5.9e-13;
Matches 244; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

QY 185 AFGTTGGATGCGAAGAGCTTAATGGGAAATTCGAAGTTGGACATTTGAATATAGGAG 244
Db 446 ATGTCGGATGCTTCAGGTCAAGTTCGGGAATTCAGAAGTAGGCGACATAAGTATAGAT 387
QY 245 CTGGAAGAGTATTTATCAAGATATTTGCGAATTAATTTGGCTGTTCAACGAACAGAT 304
Db 386 GCGGCGAGGATGCTGTTGAGATCTTTGAGAAATTAATCTTTGAGATTT-----AATGAGG 333
QY 305 TTGTTACAAATCCTCAGATTTGTCATCAGCTGAGCGTCAAGAGAGGGAGGCTGGTTCGAT 364
Db 332 TTCACAAGATCCTAAATTTGTTGAGCTTTGTCGCGGATATACAGCGAAGGCTGGGTAT 273
QY 365 TGCATTTATAGGACTGGTTAGCGAGTGGTGTCCACTCTCATATTTGATCATCTTTTTCG 424
Db 272 GCCACATGATTTGCTGCTTCTGATGTTGGAGTGCATTTCTTTCAGGCGCACATGAAA 213
QY 425 CGTTGATACGTCATTTAAACAATTTACAAGTCCCAAGGTTTTCATTTGCTGTTTTCG 484
Db 212 CCATTTAT---TGAGGTTATCACCGGATTTGGCATCAAGGTTTTTATACATGTAATTCAT 156

Db 98 AAATTGAGCACTTAAATGCCGAATTTGCTACTGTTCAGGGCGTTTACTATGCTATGATA 39
QY 605 GGGCAAAAGATGGGCGGCTTAAAGATGCTTATGA 641
Db 38 GGGATAATCCCTGGATAGGACATGTAAAGCTTATGA 2

RESULT 14
US-09-106-582-34/c
; Sequence 34, Application US/09106582
; Patent No. 6308402
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; THERAPY
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,582
; FILING DATE: 29-JUN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.439C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 484 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Ehrlichia
US-09-106-582-34

Query Match 4.7%; Score 81.4; DB 4; Length 484;
Best Local Similarity 53.4%; Pred. No. 5.9e-13;
Matches 244; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

QY 185 ATGTCGGATGCCAGAGGCTTAATGGGAAATTCGAAGTTGGACATTTGAATATAGGAG 244
Db 446 ATGTCGGATGCCCTCAGGTCAGTTCGGGAATTCAGAAATGAGGACATAGATATAGGAT 387

QY 245 CTGGAAGAGTATTTATCAAGATATTTGTCGAATTAATTTGGCTGTTCAACGAACAGAT 304
Db 386 GCGGAGGATAGTGCCTCAGGATCTTGTGAGAATTAATCTTGAGATT-----AATGAGG 333

QY 305 TTGTTACAATCTCAGATGTTCATCAGCTGAGGCTGCAAGAAGGGAGTGGTCGAT 364
Db 332 TTCACAAGATCTCAATTTGTTGACTTTGTGGCGATATACAGCGGAAGGGTGGGGTAT 273

QY 365 TGCATTTATTAGGACTGGTGTAGCGATGGTGGTGTCCACTCTCATATTTGATCATCTTTTG 424
Db 272 GCCACATGATGCTGCTCTTCTGATGGTGGAGTGCATCTCTCTCAGGCGCACATGAAA 213

QY 425 CGTTGATAGTGCATTTAAACAATTAACAAGTGCACAAAGGTTTTTCATTCATCTTTTGTG 484

Db 212 CCATTAT---TGAGGTTATCACCGGATTTGGCATCAAGGTTTTTATACATGTAATCTAG 156
QY 485 ATGCTCGAGATACTTCGCCCAACAAGTGGAGCTGTTATCTTGACAACTTCTTCAATTTA 544
Db 155 ATGCTAGGATGTT---CCACCCTGCTGCTCAGAAATATATCGGTATGCTGAACGCTA 99
QY 545 TTGCTTTCGGAAGATACGGAGAAATTTGGCTACTTACTTGACGCTTATTTATGCAATGATA 604
Db 98 AAATTGAGCACTTAAATGCCGAATTTGCTACTGTTCAGGGCGCTTACTATGCTATGATA 39
QY 605 GGGCAAAAGATGGGAGCGCTTAAAGATGCTTATGA 641
Db 38 GGGATAATCCCTGGATAGGACATGTAAAGCTTATGA 2

RESULT 15
US-09-398-395A-55
; Sequence 55, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-398-395A-55

Query Match 2.3%; Score 39.8; DB 4; Length 2861;
Best Local Similarity 53.5%; Pred. No. 0.38;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1449 AACATTTGTTTTTAATCGACTCCACTACTGAGATGATGGCAAAAGACGTCGACGAGC 1508
Db 2177 AACACGCTGCTCATATTAGTGCTCTTTTTCACCTGGGAGGTTCTTTACAGATGAAGTACTCTC 2236

QY 1509 CTTACGCTGATGTTCACCGACTGTCTTACAATTAATGGGCTTACCTGTACCGCGGAGAT 1568
Db 2237 CAAAATTGATCGGATCTAGATTCTTCAACTCATGCGCTTAACAGGGGCTTTGGTGAA 2296

QY 1569 GGATGCGGTTCTTTACTTTGAACAGAGAGATAAG 1603
Db 2297 TGACACCAAACTTATCAGCGCAGAGAGGTCAAG 2331

Search completed: August 4, 2003, 14:22:23
Job time : 97 secs